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## RAW SEQUENCE LISTING

DATE: 05/03/2002

PATENT APPLICATION: US/09/997,977

TIME: 12:01:09

Input Set : N:\Crf3\RULE60\09997977.raw

Output Set: N:\CRF3\05032002\I997977.raw

3 <110> APPLICANT: Bartel, Paul L.  
 4 Tavgigian, Sean V.  
 5 Myriad Genetics, Inc.  
 7 <120> TITLE OF INVENTION: MMSC1 - An MMAC1 Interacting Protein  
 9 <130> FILE REFERENCE: MMSC1 Gene  
 11 <140> CURRENT APPLICATION NUMBER: 09/997,977  
 12 <141> CURRENT FILING DATE: 2001-12-03  
 15 <150> PRIOR APPLICATION NUMBER: 09/233,086  
 16 <151> PRIOR FILING DATE: 1999-01-19  
 18 <150> PRIOR APPLICATION NUMBER: US 60/071,861  
 19 <151> PRIOR FILING DATE: 1998-01-20  
 21 <160> NUMBER OF SEQ ID NOS: 65  
 23 <170> SOFTWARE: PatentIn Ver. 2.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 4  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: Description of Artificial Sequence:PDZ Consensus  
 32 Domain  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: PEPTIDE  
 36 <222> LOCATION: (2)..(4)  
 37 <223> OTHER INFORMATION: Xaa at residue 2 may be Ser or Thr; Xaa at residue  
 38 3 may be any amino acid; Xaa at residue 4 may be  
 39 Val or Ile.  
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 43 1  
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 48 <212> TYPE: DNA  
 49 <213> ORGANISM: Homo sapiens  
 51 <220> FEATURE:  
 52 <221> NAME/KEY: CDS  
 53 <222> LOCATION: (115)..(5757)  
 55 <400> SEQUENCE: 2  
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 58 tgctcctcca ggcaccagg tgtctttaag agtgattgaa gagaataatt caaa atg 117  
 59 Met  
 60 1  
 62 cct gaa aat cct gct aca gat aaa ctg cag gtg ctg cag gta ctt gat 165  
 63 Pro Glu Asn Pro Ala Thr Asp Lys Leu Gln Val Leu Gln Val Leu Asp

ENTERED

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64	5	10	15	
66	cgc ctg aaa atg aaa ttg cag gag aag ggt gac acg tcg cag aat gag	213		
67	Arg Leu Lys Met Lys Leu Gln Glu Lys Gly Asp Thr Ser Gln Asn Glu			
68	20 25 30			
70	aag tta tct atg ttt tat gag aca cta aag agt cct ctc ttc aac cag	261		
71	Lys Leu Ser Met Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln			
72	35 40 45			
74	ata ctc aca ctt cag cag tcc atc aag caa ctg aag ggt caa ctc aac	309		
75	Ile Leu Thr Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly Gln Leu Asn			
76	50 55 60 65			
78	cat ata ccc tca gat tgt tca gcc aac ttt gat ttt tct agg aaa ggt	357		
79	His Ile Pro Ser Asp Cys Ser Ala Asn Phe Asp Phe Ser Arg Lys Gly			
80	70 75 80			
82	ttg tta gtg ttc aca gat ggt tcc att act aat gga aat gtc cac agg	405		
83	Leu Leu Val Phe Thr Asp Gly Ser Ile Thr Asn Gly Asn Val His Arg			
84	85 90 95			
86	ccc tct aat aac tcg act gta tct ggg tta ttt ccg tgg acc ccg aag	453		
87	Pro Ser Asn Asn Ser Thr Val Ser Gly Leu Phe Pro Trp Thr Pro Lys			
88	100 105 110			
90	ttg gga aat gaa gac ttt aac tca gtc att caa cag atg gct cag ggc	501		
91	Leu Gly Asn Glu Asp Phe Asn Ser Val Ile Gln Gln Met Ala Gln Gly			
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94	cgg caa att gaa tat ata gat ata gaa cgg cct tca act gga ggc ctt	549		
95	Arg Gln Ile Glu Tyr Ile Asp Ile Glu Arg Pro Ser Thr Gly Gly Leu			
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98	gga ttc agt gtg gtg gcc ctc aga agt caa aat ctc gga aaa gtt gat	597		
99	Gly Phe Ser Val Val Ala Leu Arg Ser Gln Asn Leu Gly Lys Val Asp			
100	150 155 160			
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103	Ile Phe Val Lys Asp Val Gln Pro Gly Ser Val Ala Asp Arg Asp Gln			
104	165 170 175			
106	aga tta aag gaa aat gat caa ata ttg gcc att aat cac acg cca ttg	693		
107	Arg Leu Lys Glu Asn Asp Gln Ile Leu Ala Ile Asn His Thr Pro Leu			
108	180 185 190			
110	gat cag aac att tcc cat cag caa gca att gca tta tta caa caa acc	741		
111	Asp Gln Asn Ile Ser His Gln Gln Ala Ile Ala Leu Leu Gln Gln Thr			
112	195 200 205			
114	act gga tct ttg aga ctg att gtg gcc agg gaa cca gtc cac aca aaa	789		
115	Thr Gly Ser Leu Arg Leu Ile Val Ala Arg Glu Pro Val His Thr Lys			
116	210 215 220 225			
118	agc agt act tct agc agc cta aat gat aca act ctg cct gaa aca gtt	837		
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122	tgt tgg ggc cat gtt gaa gag gtt gag ctc att aat gat ggc tct gga	885		
123	Cys Trp Gly His Val Glu Glu Val Glu Leu Ile Asn Asp Gly Ser Gly			
124	245 250 255			
126	cta ggt ttt gga ata gtt gga gga aaa aca agt ggc gtg gtt gtg agg	933		
127	Leu Gly Phe Gly Ile Val Gly Gly Lys Thr Ser Gly Val Val Val Arg			
128	260 265 270			

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130 act ata gtt cct gga gga tta gca gat cga gat gga aga ctc cag aca 981
131 Thr Ile Val Pro Gly Gly Leu Ala Asp Arg Asp Gly Arg Leu Gln Thr
132 275 280 285
134 ggg gac cac atc ttg aag att ggt ggc aca aac gtg cag gga atg acc 1029
135 Gly Asp His Ile Leu Lys Ile Gly Gly Thr Asn Val Gln Gly Met Thr
136 290 295 300 305
138 agt gag caa gtt gca caa gtt cta agg aac tgt ggg aat tca gtc agg 1077
139 Ser Glu Gln Val Ala Gln Val Leu Arg Asn Cys Gly Asn Ser Val Arg
140 310 315 320
142 atg ctc gtt gct aga gat cca gct ggt gac att tca gtc acc ccc cct 1125
143 Met Leu Val Ala Arg Asp Pro Ala Gly Asp Ile Ser Val Thr Pro Pro
144 325 330 335
146 gcc cct gca gcc tta cct gtt gcc ctg cct act gta gcc agc aag ggc 1173
147 Ala Pro Ala Ala Leu Pro Val Ala Leu Pro Thr Val Ala Ser Lys Gly
148 340 345 350
150 cct ggt tct gac agt tct ctt ttt gaa act tat aat gtt gag ctt gtg 1221
151 Pro Gly Ser Asp Ser Ser Leu Phe Glu Thr Tyr Asn Val Glu Leu Val
152 355 360 365
154 aga aaa gat ggg cag agt ctt gga att aga att gtt ggc tat gtt gga 1269
155 Arg Lys Asp Gly Gln Ser Leu Gly Ile Arg Ile Val Gly Tyr Val Gly
156 370 375 380 385
158 aca tct cat aca ggg gaa gct tca ggg att tat gtg aaa agt gta ata 1317
159 Thr Ser His Thr Gly Glu Ala Ser Gly Ile Tyr Val Lys Ser Val Ile
160 390 395 400
162 cct ggc agt gct gcg tac cac aat ggc cac att caa gtg aat gac aaa 1365
163 Pro Gly Ser Ala Ala Tyr His Asn Gly His Ile Gln Val Asn Asp Lys
164 405 410 415
166 ata gtt gct gtc gat ggc gtg aac att cag ggt ttt gcc aac cat gat 1413
167 Ile Val Ala Val Asp Gly Val Asn Ile Gln Gly Phe Ala Asn His Asp
168 420 425 430
170 gtt gtt gaa gta tta cga aat gca ggg cag gtg gta cac cta acc cta 1461
171 Val Val Glu Val Leu Arg Asn Ala Gly Gln Val Val His Leu Thr Leu
172 435 440 445
174 gtt cga agg aag aca tcc tca tct act tct cca ctt gaa cca cct tca 1509
175 Val Arg Arg Lys Thr Ser Ser Ser Thr Ser Pro Leu Glu Pro Pro Ser
176 450 455 460 465
178 gac aga gga act gtt gta gaa cca ctg aaa cca cca gct ctc ttt cta 1557
179 Asp Arg Gly Thr Val Val Glu Pro Leu Lys Pro Pro Ala Leu Phe Leu
180 470 475 480
182 act gga gca gtg gaa act gaa act aat gtg gat ggt gaa gat gag gaa 1605
183 Thr Gly Ala Val Glu Thr Glu Thr Asn Val Asp Gly Glu Asp Glu Glu
184 485 490 495
186 att aaa gaa aga att gat act tta aaa aat gac aac ata caa gcc tta 1653
187 Ile Lys Glu Arg Ile Asp Thr Leu Lys Asn Asp Asn Ile Gln Ala Leu
188 500 505 510
190 gaa aaa ttg gaa aaa gtc cca gac tct cca gaa aat gag ctg aaa tcc 1701
191 Glu Lys Leu Glu Lys Val Pro Asp Ser Pro Glu Asn Glu Leu Lys Ser
192 515 520 525
194 aga tgg gaa aac ctg ttg ggt cct gat tat gaa gta atg gtt gct act 1749

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199	Leu	Asp	Thr	Gln	Ile	Ala	Asp	Asp	Ala	Glu	Leu	Gln	Lys	Tyr	Ser	Lys	
200					550					555						560	
202	ctg	ctg	cct	att	cac	act	ctg	agg	ctt	ggt	gtg	gaa	gtg	gat	tcc	ttt	1845
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206	gat	ggg	cac	cat	tat	att	tct	tca	att	gtt	tct	ggt	ggt	cct	gtt	gat	1893
207	Asp	Gly	His	His	Tyr	Ile	Ser	Ser	Ile	Val	Ser	Gly	Gly	Pro	Val	Asp	
208					580					585						590	
210	aca	ttg	ggt	ctc	cta	cag	cca	gaa	gat	gag	ctg	ctt	gag	gtc	aat	ggc	1941
211	Thr	Leu	Gly	Leu	Leu	Gln	Pro	Glu	Asp	Glu	Leu	Leu	Glu	Val	Asn	Gly	
212					595					600						605	
214	atg	cag	ctt	tat	gga	aaa	tct	cgc	cga	gaa	gca	gtc	tcc	ttt	ctt	aaa	1989
215	Met	Gln	Leu	Tyr	Gly	Lys	Ser	Arg	Arg	Glu	Ala	Val	Ser	Phe	Leu	Lys	
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218	gaa	gtg	cca	ccc	cct	ttt	act	ttg	gtt	tgc	tgt	cgg	agg	ttg	ttt	gat	2037
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226	gag	aca	gag	gtt	gac	cac	aat	atg	gat	gtc	aat	act	gaa	gaa	gat	gat	2133
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234	gta	aaa	gat	tgt	aaa	ggt	ttg	gga	ttc	agc	att	ttg	gat	tac	cag	gac	2229
235	Val	Lys	Asp	Cys	Lys	Gly	Leu	Gly	Phe	Ser	Ile	Leu	Asp	Tyr	Gln	Asp	
236	690					695						700				705	
238	cct	tta	gat	cct	aca	aga	tca	gtg	att	gtg	atc	cgc	tcc	ctg	gta	gca	2277
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240					710							715				720	
242	gat	ggt	gta	gca	gaa	aga	agt	ggg	gga	cta	tta	cct	gga	gac	cgc	ctg	2325
243	Asp	Gly	Val	Ala	Glu	Arg	Ser	Gly	Gly	Leu	Leu	Pro	Gly	Asp	Arg	Leu	
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246	gtc	tca	gtc	aat	gaa	tac	tgt	ttg	gac	aac	acc	tca	ctt	gct	gaa	gct	2373
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250	gtg	gaa	ata	ttg	aaa	gct	gtg	cca	cca	ggc	cta	gta	cac	ctt	ggc	atc	2421
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254	tgt	aag	cct	ttg	gtg	gaa	gat	aat	gaa	gaa	gaa	agt	tgt	tat	att	tta	2469
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256	770					775						780				785	
258	cat	tca	agc	agt	aat	gaa	gac	aag	act	gaa	ttt	tca	gga	aca	att	cat	2517
259	His	Ser	Ser	Ser	Asn	Glu	Asp	Lys	Thr	Glu	Phe	Ser	Gly	Thr	Ile	His	

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260		790		795		800	
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267	Glu	Pro	Tyr	Phe	Lys	Glu	Leu
268			820			825	
270	gga	aag	tct	ttc	cat	tcc	caa
271	Gly	Lys	Ser	Phe	His	Ser	Gln
272			835			840	
274	gcc	tgg	gag	atg	cat	gaa	ttt
275	Ala	Trp	Glu	Met	His	Glu	Phe
276	850					855	
278	gaa	gaa	aga	gaa	atg	ctt	ggt
279	Glu	Glu	Arg	Glu	Met	Leu	Val
280						870	
282	ccc	tca	cca	tcc	atg	gag	ttg
283	Pro	Ser	Pro	Ser	Met	Glu	Leu
284						885	
286	act	cct	gtg	ccc	tct	gtg	aat
287	Thr	Pro	Val	Pro	Ser	Val	Asn
288			900			905	
290	cat	gat	aat	gaa	cca	tcc	gag
291	His	Asp	Asn	Glu	Pro	Ser	Glu
292			915			920	
294	gtc	tat	tcc	cag	gag	gca	cag
295	Val	Tyr	Ser	Gln	Glu	Ala	Gln
296	930					935	
298	atg	aaa	gaa	aat	ttt	gtc	atg
299	Met	Lys	Glu	Asn	Phe	Val	Met
300						950	
302	gaa	gga	aac	agt	caa	caa	ggc
303	Glu	Gly	Asn	Ser	Gln	Gln	Gly
304						965	
306	tca	tta	gca	aaa	act	agt	ctg
307	Ser	Leu	Ala	Lys	Thr	Ser	Leu
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310	caa	ggt	cct	agc	ttg	ctc	att
311	Gln	Gly	Pro	Ser	Leu	Leu	Ile
312			995			1000	
314	gag	caa	gaa	gat	ttg	cct	tta
315	Glu	Gln	Glu	Asp	Leu	Pro	Leu
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318	tcc	aag	gcc	tca	gca	tac	aca
319	Ser	Lys	Ala	Ser	Ala	Tyr	Thr
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323	Asp	Thr	Cys	Glu	Leu	Pro	Glu
324						1045	

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3,4

VERIFICATION SUMMARY

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L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0